

SEQUENCE LISTING

<110> MIYATA, TOSHIO
KUROKAWA, KIYOSHI

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<150> JP 1999-233301

<151> 1999-08-19

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (23).. (2872)

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Leu Gln Glu Asp Ala Asp Gly Phe Gly Val Asp Asp Tyr Ser Ser Glu
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Ser Asp Val Ile Ile Ile Pro Ser Ala Leu Asp Phe Val Ser Gln Asp
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Glu Met Leu Thr Pro Leu Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu
45 50 55

aac ata ttt aac aga caa atg gtg gcc cgg agt ttg ctc gat acc ttg 244
Asn Ile Phe Asn Arg Gln Met Val Ala Arg Ser Leu Leu Asp Thr Leu
60 65 70

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Arg Glu Val Cys Asp Asp Glu Arg Asp Cys Ile Ala Val Leu Glu Arg	
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Ile Ser Arg Leu Ala Asp Asp Ser Glu Pro Thr Val Arg Ala Glu Leu	
95 100 105	
atg gaa cag gtg cct cac atc gca ctg ttt tgt caa gaa aac cgg cct	388
Met Glu Gln Val Pro His Ile Ala Leu Phe Cys Gln Glu Asn Arg Pro	
110 115 120	
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Ser Ile Pro Tyr Ala Phe Ser Lys Phe Leu Leu Pro Ile Val Val Arg	
125 130 135	
tac ctt gca gat cag aat aat cag gtg agg aaa aca agt cag gca gct	484
Tyr Leu Ala Asp Gln Asn Asn Gln Val Arg Lys Thr Ser Gln Ala Ala	
140 145 150	
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Leu Leu Ala Leu Leu Glu Gln Glu Leu Ile Glu Arg Phe Asp Val Glu	
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acc aaa gtg tgg cct gtc ctc ata gag ctg aca gcc cca gat agc aat	580
Thr Lys Val Trp Pro Val Leu Ile Glu Leu Thr Ala Pro Asp Ser Asn	
175 180 185	
gat gat gtg aaa aca gaa gct gtg gct ata atg tgc aaa atg gct ccc	628
Asp Asp Val Lys Thr Glu Ala Val Ala Ile Met Cys Lys Met Ala Pro	
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Met Val Gly Lys Asp Ile Thr Glu Arg Leu Ile Leu Pro Arg Phe Cys	
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Glu Met Cys Cys Asp Cys Arg Met Phe His Val Arg Lys Val Cys Ala	
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Ala Asn Phe Gly Asp Ile Cys Ser Val Val Gly Gln Gln Ala Thr Glu	
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Glu Met Leu Leu Pro Arg Phe Phe Gln Leu Cys Ser Asp Asn Val Trp	
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Gly Val Arg Lys Ala Cys Ala Glu Cys Phe Met Ala Val Ser Cys Ala	
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Thr Cys Gln Glu Ile Arg Arg Thr Lys Leu Ser Ala Leu Phe Ile Asn	
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Tyr Phe Lys Glu Glu Ser Lys Ser Ser Glu Glu Met Ser Val Glu Asn	
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Lys Asn Arg Thr Arg Asp Gln Glu Ala Pro Glu Asp Val Gln Val Arg	
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Pro Glu Asp Thr Pro Ser Asp Leu Ser Val Ser Asn Ser Ser Val Ile	
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Leu Glu Asn Thr Met Glu Asp His Ala Ala Glu Ala Ser Gly Lys Pro	
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Leu Gly Glu Ile Ser Val Pro Leu Asp Ser Ser Leu Leu Cys Thr Leu	
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415 420 425	
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Pro Gly Asn Tyr Lys Ser Met Leu Arg Pro Glu Val Gly Thr Thr Ser	
430 435 440	
caa gat tca gct ctc tta gat cag gaa ttg tat aac tcc ttc cat ttc	1396
Gln Asp Ser Ala Leu Leu Asp Gln Glu Leu Tyr Asn Ser Phe His Phe	
445 450 455	

tgg agg act cct ctt cct gaa ata gat cta gac ata gag ctt gaa cag	1444
Trp Arg Thr Pro Leu Pro Glu Ile Asp Leu Asp Ile Glu Leu Glu Gln	
460 465 470	
aac tct ggg gga aaa ccc agc cca gag gga cca gag gaa gaa tct gag	1492
Asn Ser Gly Gly Lys Pro Ser Pro Glu Gly Pro Glu Glu Glu Ser Glu	
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Gly Pro Val Pro Ser Ser Pro Asn Ile Thr Met Ala Thr Arg Lys Glu	
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ctg gaa gaa atg ata gaa aat cta gag ccc cac att gat gat cca gat	1588
Leu Glu Glu Met Ile Glu Asn Leu Glu Pro His Ile Asp Asp Pro Asp	
510 515 520	
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Val Lys Ala Gln Val Glu Val Leu Ser Ala Ala Leu Arg Ala Ser Ser	
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Gln Asp Glu Leu Asp Ile Asn Glu Leu Pro Asn Cys Lys Ile Asn Gln	
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Glu Asp Ser Val Pro Leu Ile Ser Asp Ala Val Glu Asn Met Asp Ser	
575 580 585	
act ctt cac tat att cac aac gat tca gac ttg agc aac aat agc agt	1828
Thr Leu His Tyr Ile His Asn Asp Ser Asp Leu Ser Asn Asn Ser Ser	
590 595 600	
ttt agc cct gat gag gaa agg aga act aaa gta caa gat gtt gta cct	1876
Phe Ser Pro Asp Glu Glu Arg Arg Thr Lys Val Gln Asp Val Val Pro	
605 610 615	
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Gln Ala Leu Leu Asp Gln Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala	
620 625 630	
cag acg gtt gac act gaa att gct aag cac tgt gca tat agc ctc cct	1972
Gln Thr Val Asp Thr Glu Ile Ala Lys His Cys Ala Tyr Ser Leu Pro	
635 640 645 650	

ggt gtg gcc ttg aca ctc gga aga cag aat tgg cac tgc ctg aga gag	2020
Gly Val Ala Leu Thr Leu Gly Arg Gln Asn Trp His Cys Leu Arg Glu	
655 660 665	
acg tat gag act ctg gcc tca gac atg cag tgg aaa gtt cga cga act	2068
Thr Tyr Glu Thr Leu Ala Ser Asp Met Gln Trp Lys Val Arg Arg Thr	
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cta gca ttc tcc atc cac gag ctt gca gtt att ctt gga gat caa ttg	2116
Leu Ala Phe Ser Ile His Glu Leu Ala Val Ile Leu Gly Asp Gln Leu	
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Asp Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys	
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Ala Glu Gln Leu Ile Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val	
765 770 775	
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Lys Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn	
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Glu Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln	
830 835 840	

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gcc ttt gtc ttt gtc tgc cag act gtc att gag gat gac tgc ctt ccc 2596
 Ala Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro
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atg gac cag ttt gct gtg cat ctc atg ccg cat ctg cta acc tta gca 2644
 Met Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala
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aat gac agg gtt cct aac gtg cga gtg ctg ctt gca aag aca tta aga 2692
 Asn Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg
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caa act cta cta gaa aaa gac tat ttc ttg gcc tct gcc agc tgc cac 2740
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 Ser Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile
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tcc gaa gat gcc atg agc aca gcg tcc tca acc tac tagaaggctt 2882
 Ser Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr
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<213> Homo sapiens

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35 40 45

Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu Asn Ile Phe Asn Arg Gln
50 55 60

Met Val Ala Arg Ser Leu Leu Asp Thr Leu Arg Glu Val Cys Asp Asp
65 70 75 80

Glu Arg Asp Cys Ile Ala Val Leu Glu Arg Ile Ser Arg Leu Ala Asp
85 90 95

Asp Ser Glu Pro Thr Val Arg Ala Glu Leu Met Glu Gln Val Pro His
100 105 110

Ile Ala Leu Phe Cys Gln Glu Asn Arg Pro Ser Ile Pro Tyr Ala Phe
115 120 125

Ser Lys Phe Leu Leu Pro Ile Val Val Arg Tyr Leu Ala Asp Gln Asn
130 135 140

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Gln	Glu	Leu	Ile	Glu	Arg	Phe	Asp	Val	Glu	Thr	Lys	Val	Trp	Pro	Val
				165					170					175	
Leu	Ile	Glu	Leu	Thr	Ala	Pro	Asp	Ser	Asn	Asp	Asp	Val	Lys	Thr	Glu
			180					185					190		
Ala	Val	Ala	Ile	Met	Cys	Lys	Met	Ala	Pro	Met	Val	Gly	Lys	Asp	Ile
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Thr	Glu	Arg	Leu	Ile	Leu	Pro	Arg	Phe	Cys	Glu	Met	Cys	Cys	Asp	Cys
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Arg	Met	Phe	His	Val	Arg	Lys	Val	Cys	Ala	Ala	Asn	Phe	Gly	Asp	Ile
225					230					235					240
Cys	Ser	Val	Val	Gly	Gln	Gln	Ala	Thr	Glu	Glu	Met	Leu	Leu	Pro	Arg
				245					250					255	
Phe	Phe	Gln	Leu	Cys	Ser	Asp	Asn	Val	Trp	Gly	Val	Arg	Lys	Ala	Cys
			260					265					270		
Ala	Glu	Cys	Phe	Met	Ala	Val	Ser	Cys	Ala	Thr	Cys	Gln	Glu	Ile	Arg
		275					280					285			
Arg	Thr	Lys	Leu	Ser	Ala	Leu	Phe	Ile	Asn	Leu	Ile	Ser	Asp	Pro	Ser
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Arg	Trp	Val	Arg	Gln	Ala	Ala	Phe	Gln	Ser	Leu	Gly	Pro	Phe	Ile	Ser
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Thr	Phe	Ala	Asn	Pro	Ser	Ser	Ser	Gly	Gln	Tyr	Phe	Lys	Glu	Glu	Ser
				325					330					335	
Lys	Ser	Ser	Glu	Glu	Met	Ser	Val	Glu	Asn	Lys	Asn	Arg	Thr	Arg	Asp
			340					345					350		
Gln	Glu	Ala	Pro	Glu	Asp	Val	Gln	Val	Arg	Pro	Glu	Asp	Thr	Pro	Ser
		355					360					365			
Asp	Leu	Ser	Val	Ser	Asn	Ser	Ser	Val	Ile	Leu	Glu	Asn	Thr	Met	Glu
	370					375					380				
Asp	His	Ala	Ala	Glu	Ala	Ser	Gly	Lys	Pro	Leu	Gly	Glu	Ile	Ser	Val
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Pro Leu Asp Ser Ser Leu Leu Cys Thr Leu Ser Ser Glu Ser His Gln
405 410 415

Glu Ala Ala Ser Asn Glu Asn Asp Lys Lys Pro Gly Asn Tyr Lys Ser
420 425 430

Met Leu Arg Pro Glu Val Gly Thr Thr Ser Gln Asp Ser Ala Leu Leu
435 440 445

Asp Gln Glu Leu Tyr Asn Ser Phe His Phe Trp Arg Thr Pro Leu Pro
450 455 460

Glu Ile Asp Leu Asp Ile Glu Leu Glu Gln Asn Ser Gly Gly Lys Pro
465 470 475 480

Ser Pro Glu Gly Pro Glu Glu Glu Ser Glu Gly Pro Val Pro Ser Ser
485 490 495

Pro Asn Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu
500 505 510

Asn Leu Glu Pro His Ile Asp Asp Pro Asp Val Lys Ala Gln Val Glu
515 520 525

Val Leu Ser Ala Ala Leu Arg Ala Ser Ser Leu Asp Ala His Glu Glu
530 535 540

Thr Ile Ser Ile Glu Lys Arg Ser Asp Leu Gln Asp Glu Leu Asp Ile
545 550 555 560

Asn Glu Leu Pro Asn Cys Lys Ile Asn Gln Glu Asp Ser Val Pro Leu
565 570 575

Ile Ser Asp Ala Val Glu Asn Met Asp Ser Thr Leu His Tyr Ile His
580 585 590

Asn Asp Ser Asp Leu Ser Asn Asn Ser Ser Phe Ser Pro Asp Glu Glu
595 600 605

Arg Arg Thr Lys Val Gln Asp Val Val Pro Gln Ala Leu Leu Asp Gln
610 615 620

Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala Gln Thr Val Asp Thr Glu
625 630 635 640

Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala Leu Thr Leu
645 650 655

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Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu Thr Leu Ala
 660 665 670

Ser Asp Met Gln Trp Lys Val Arg Arg Thr Leu Ala Phe Ser Ile His
 675 680 685

Glu Leu Ala Val Ile Leu Gly Asp Gln Leu Thr Ala Ala Asp Leu Val
 690 695 700

Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp Glu Val Arg Ile Gly
 705 710 715 720

Val Leu Lys His Leu His Asp Phe Leu Lys Leu Leu His Ile Asp Lys
 725 730 735

Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe Leu Val Thr Asp Asn
 740 745 750

Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala Glu Gln Leu Ile Leu
 755 760 765

Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr Asp Tyr Leu Arg Pro
 770 775 780

Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser Ser Val Arg Trp Ile
 785 790 795 800

Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys Leu His Ala Ala Thr
 805 810 815

Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu Leu Val Glu Asn Phe
 820 825 830

Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala Phe Val Phe Val Cys
 835 840 845

Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln Phe Ala Val
 850 855 860

His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg Val Pro Asn
 865 870 875 880

Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu Leu Glu Lys
 885 890 895

Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala Val Glu Gln
 900 905 910

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Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val Lys Tyr Phe
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Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser Glu Asp Ala Met Ser
930 935 940

Thr Ala Ser Ser Thr Tyr
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<210> 3
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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tgtaaaacga cggccagt 18

<210> 4
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<213> Artificial Sequence

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Synthesized Primer Sequence

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<210> 5
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<220>
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Synthesized Primer Sequence

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<400> 5
tcagagaggt cattc 15

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Synthesized Primer Sequence

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<210> 10

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<221> CDS

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10

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96

Ala Asp Gly Leu Gly Val Asp Asp Tyr Ser Ser Glu Ser Asp Val Ile

15

20

25

30

att ata cct tca gcc ctg gac ttc gtc tca caa gat gaa atg ttg aca

144

Ile Ile Pro Ser Ala Leu Asp Phe Val Ser Gln Asp Glu Met Leu Thr

35

40

45

ccc ttg ggg agg ctg gac aag tat gct gca agt gag aac gtc ttt aac

192

Pro Leu Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu Asn Val Phe Asn

50

55

60

cag gaa atg ttc aac tcc ttc cat ttc tgg agg act cct cta ccc cag Gln Glu Met Phe Asn Ser Phe His Phe Trp Arg Thr Pro Leu Pro Gln 450 455 460	1392
ata gat ctt gat aaa gag ctc caa cag gac cct ggg gag agg ccc agc Ile Asp Leu Asp Lys Glu Leu Gln Gln Asp Pro Gly Glu Arg Pro Ser 465 470 475	1440
cca gag aga aca gga gat gca cct gca gcc cct gta cca ggt tct ccc Pro Glu Arg Thr Gly Asp Ala Pro Ala Ala Pro Val Pro Gly Ser Pro 480 485 490	1488
agt atc acc atg gct acc cgg aag gaa cta gaa gaa atg ata gaa aac Ser Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu Asn 495 500 505 510	1536
cta gag ccg cac atg gat gac ccg gat gtt aaa gcc cag gtg gaa gtg Leu Glu Pro His Met Asp Asp Pro Asp Val Lys Ala Gln Val Glu Val 515 520 525	1584
ctg tcg gcc gcc ctg cgc gct tct acc ctg gat gct cac gac gag gct Leu Ser Ala Ala Leu Arg Ala Ser Thr Leu Asp Ala His Asp Glu Ala 530 535 540	1632
ggc ggt gca gag cag cgg agt gag ctg cag gac gac gca gtg ggt gcc Gly Gly Ala Glu Gln Arg Ser Glu Leu Gln Asp Asp Ala Val Gly Ala 545 550 555	1680
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cat gga ggt gcg gat gta ggc ccc ggt ggc ggt ggt ggc ttc agc ccg His Gly Gly Ala Asp Val Gly Pro Gly Gly Gly Gly Gly Phe Ser Pro 595 600 605	1824
gat gaa gag agg aga ccc aaa gtc cag gat gtc gta cca caa gcg tta Asp Glu Glu Arg Arg Pro Lys Val Gln Asp Val Val Pro Gln Ala Leu 610 615 620	1872
cta gac cag tac ctg tca atg acc gac cct tct cga gca cag aca gtc Leu Asp Gln Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala Gln Thr Val 625 630 635	1920

gac acc gag atc gct aag cac tgt gca tac agt ctg ccg ggt gtg gct Asp Thr Glu Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala 640 645 650	1968
ctg acc ctt ggc aga cag aac tgg cac tgc ttg aga gag act tac gag Leu Thr Leu Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu 655 660 665 670	2016
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tta cgt ccc att gct ctg aat ctg tgt gca gac aaa gtt tct tca gtc Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser Ser Val 785 790 795	2400
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Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg	
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Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu	
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Leu Glu Lys Glu Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala	
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Lys Tyr Phe Ala Ser Ile His Pro Ser Ser Thr Lys Leu Ser Glu Asp	
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<213> RATTUS NORVEGICUS

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Ser Lys Tyr Leu Leu Pro Ile Val Val Arg Tyr Leu Ala Asp Gln Asn
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Gln Glu Leu Ile Glu Arg Leu Asp Val Glu Thr Lys Val Cys Pro Val
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	275		280		285	
Arg Thr Lys Leu Ser Ala Leu Phe Ile Asn Leu Ile Ser Asp Pro Ser						
	290		295		300	
Arg Trp Val Arg Gln Ala Ala Phe Gln Ser Leu Gly Pro Phe Ile Ser						
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Thr Phe Ala Asn Pro Ser Ser Ser Gly Gln Cys Phe Lys Asp Glu Ser						
	325		330		335	
Lys Ser Ser Glu Asp Lys Asp Arg Ile Arg Asp Asp Gly Val Val Gln						
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	355		360		365	
His Ser Ser Ala Arg Leu Asp Gly Thr Leu Glu Gly Cys Ala Ala Glu						
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385		390		395		400
Leu Leu Cys Thr Leu Ser Ser Glu Ser Pro Gln Glu Ala Ala Ser Asp						
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Arg Thr Gly Asp Ala Pro Ala Ala Pro Val Pro Gly Ser Pro Ser Ile						

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Ala Glu Gln Arg Ser Glu Leu Gln Asp Asp Ala Val Gly Ala Gly Gly		
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565	570	575
Ile Ala Ala Glu Glu Asn Met Glu Ala Thr Pro Asp Tyr Ile His Gly		
580	585	590
Gly Ala Asp Val Gly Pro Gly Gly Gly Gly Gly Phe Ser Pro Asp Glu		
595	600	605
Glu Arg Arg Pro Lys Val Gln Asp Val Val Pro Gln Ala Leu Leu Asp		
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Gln Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala Gln Thr Val Asp Thr		
625	630	635
Glu Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala Leu Thr		
645	650	655
Leu Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu Thr Leu		
660	665	670
Ala Ser Asp Met Gln Trp Lys Val Arg Arg Thr Leu Ala Phe Ser Ile		
675	680	685
His Glu Leu Ala Val Ile Leu Gly Asp Gln Leu Thr Ala Ala Asp Leu		
690	695	700
Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp Glu Val Arg Ile		
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Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu Leu His Ile Asp		
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Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe Leu Val Thr Asp		

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740	745	750
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Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln Phe Ala		
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Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val Lys Tyr		
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tcagaagaca aagacaggat cagagacgat ggtgtttgtac aagaagagca gagcaggcca	240
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KUROKAWA, KIYOSHI

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Ser Asp Val Ile Ile Ile Pro Ser Ala Leu Asp Phe Val Ser Gln Asp
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Ser Ile Pro Tyr Ala Phe Ser Lys Phe Leu Leu Pro Ile Val Val Arg	
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Met Val Gly Lys Asp Ile Thr Glu Arg Leu Ile Leu Pro Arg Phe Cys	
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Lys Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn	
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Glu Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln	
830 835 840	
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Met Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala	
860 865 870	
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Asn Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg	
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Gln Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His	
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Gln Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp	
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agc gat gtc aag tat ttt gca agc atc cac cct gcc agt acc aaa atc	2836
Ser Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile	
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Ser Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr	
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 <212> PRT
 <213> Homo sapiens

<400> 2

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Glu	Arg	Asp	Cys	Ile	Ala	Val	Leu	Glu	Arg	Ile	Ser	Arg	Leu	Ala	Asp
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Asp	Ser	Glu	Pro	Thr	Val	Arg	Ala	Glu	Leu	Met	Glu	Gln	Val	Pro	His
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Phe	Phe	Gln	Leu	Cys	Ser	Asp	Asn	Val	Trp	Gly	Val	Arg	Lys	Ala	Cys		
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Lys	Ser	Ser	Glu	Glu	Met	Ser	Val	Glu	Asn	Lys	Asn	Arg	Thr	Arg	Asp		
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Asp	His	Ala	Ala	Glu	Ala	Ser	Gly	Lys	Pro	Leu	Gly	Glu	Ile	Ser	Val		
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Pro	Leu	Asp	Ser	Ser	Leu	Leu	Cys	Thr	Leu	Ser	Ser	Glu	Ser	His	Gln		
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Glu	Ala	Ala	Ser	Asn	Glu	Asn	Asp	Lys	Lys	Pro	Gly	Asn	Tyr	Lys	Ser		
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Asp	Gln	Glu	Leu	Tyr	Asn	Ser	Phe	His	Phe	Trp	Arg	Thr	Pro	Leu	Pro		
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 Ser Pro Glu Gly Pro Glu Glu Glu Ser Glu Gly Pro Val Pro Ser Ser
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 Pro Asn Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu
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 Asn Leu Glu Pro His Ile Asp Asp Pro Asp Val Lys Ala Gln Val Glu
 515 520 525
 Val Leu Ser Ala Ala Leu Arg Ala Ser Ser Leu Asp Ala His Glu Glu
 530 535 540
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 595 600 605
 Arg Arg Thr Lys Val Gln Asp Val Val Pro Gln Ala Leu Leu Asp Gln
 610 615 620
 Tyr Leu Ser Met Thr Asp Pro Ser Arg Ala Gln Thr Val Asp Thr Glu
 625 630 635 640
 Ile Ala Lys His Cys Ala Tyr Ser Leu Pro Gly Val Ala Leu Thr Leu
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 Gly Arg Gln Asn Trp His Cys Leu Arg Glu Thr Tyr Glu Thr Leu Ala
 660 665 670
 Ser Asp Met Gln Trp Lys Val Arg Arg Thr Leu Ala Phe Ser Ile His
 675 680 685
 Glu Leu Ala Val Ile Leu Gly Asp Gln Leu Thr Ala Ala Asp Leu Val
 690 695 700
 Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp Glu Val Arg Ile Gly
 705 710 715 720
 Val Leu Lys His Leu His Asp Phe Leu Lys Leu Leu His Ile Asp Lys
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 Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe Leu Val Thr Asp Asn
 740 745 750
 Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala Glu Gln Leu Ile Leu
 755 760 765

Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr Asp Tyr Leu Arg Pro
770 775 780

Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser Ser Val Arg Trp Ile
785 790 795 800

Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys Leu His Ala Ala Thr
805 810 815

Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu Leu Val Glu Asn Phe
820 825 830

Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala Phe Val Phe Val Cys
835 840 845

Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln Phe Ala Val
850 855 860

His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg Val Pro Asn
865 870 875 880

Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu Leu Glu Lys
885 890 895

Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala Val Glu Gln
900 905 910

Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val Lys Tyr Phe
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Thr Ala Ser Ser Thr Tyr
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Synthesized Primer Sequence

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21

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<223> 5'-phosphorylation

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Gly Glu Glu Arg Asp Cys Ile Ala Val Leu Glu Arg Ile Ser Arg Leu	
80 85 90	
gct gat gac tca gaa cca acc gtg aga gcc gag ctg atg gaa cag gtg	336
Ala Asp Asp Ser Glu Pro Thr Val Arg Ala Glu Leu Met Glu Gln Val	
95 100 105 110	
ccg cac atc gca ctg ttt tgt caa gag aac cga cct tcc ata cca tat	384
Pro His Ile Ala Leu Phe Cys Gln Glu Asn Arg Pro Ser Ile Pro Tyr	
115 120 125	
gcc ttt tcc aag tac tta ctg cca atc gtg gtt aga tac ctt gca gac	432
Ala Phe Ser Lys Tyr Leu Leu Pro Ile Val Val Arg Tyr Leu Ala Asp	
130 135 140	
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Gln Asn Asn Gln Val Arg Lys Thr Ser Gln Ala Ala Leu Leu Ala Leu	
145 150 155	
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Leu Glu Gln Glu Leu Ile Glu Arg Leu Asp Val Glu Thr Lys Val Cys	
160 165 170	
ccc gtc ctc ata gac ttg act gcc cca gac agc aat gac gat gtg aag	576
Pro Val Leu Ile Asp Leu Thr Ala Pro Asp Ser Asn Asp Asp Val Lys	
175 180 185 190	
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Thr Glu Ala Val Ala Ile Met Cys Lys Met Ala Pro Met Val Gly Lys	
195 200 205	
gat att aca gag cgt ctc atc ctc cct agg ttt tgt gag atg tgc tgt	672
Asp Ile Thr Glu Arg Leu Ile Leu Pro Arg Phe Cys Glu Met Cys Cys	
210 215 220	
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Asp Ile Cys Ser Val Val Gly Gln Gln Ala Thr Glu Glu Met Leu Leu	
240 245 250	
ccc agg ttc ttc cag ctg tgt tct gac aat gtg tgg ggc gtc cgg aag	816
Pro Arg Phe Phe Gln Leu Cys Ser Asp Asn Val Trp Gly Val Arg Lys	
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275 280 285	

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Ile Arg Arg Thr Lys Leu Ser Ala Leu Phe Ile Asn Leu Ile Ser Asp	
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Ile Ser Thr Phe Ala Asn Pro Ser Ser Ser Gly Gln Cys Phe Lys Asp	
320 325 330	
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Glu Ser Lys Ser Ser Gln Asp Lys Asp Arg Ile Arg Asp Asp Gly Val	
335 340 345 350	
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Val Gln Glu Glu Gln Ser Arg Pro Glu Asp Ala Pro Ser Asp Leu Ser	
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Ser Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu Asn	
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 Met Ala Asp Leu Ser Leu Leu Gln Glu Asp Leu Pro Glu Asp Ala Asp
 1 5 10 15
 Gly Leu Gly Val Asp Asp Tyr Ser Ser Glu Ser Asp Val Ile Ile Ile
 20 25 30
 Pro Ser Ala Leu Asp Phe Val Ser Gln Asp Glu Met Leu Thr Pro Leu
 35 40 45
 Gly Arg Leu Asp Lys Tyr Ala Ala Ser Glu Asn Val Phe Asn Arg Gln
 50 55 60
 Met Val Ala Arg Ser Leu Leu Asp Thr Leu Arg Glu Val Cys Gly Glu
 65 70 75 80
 Glu Arg Asp Cys Ile Ala Val Leu Glu Arg Ile Ser Arg Leu Ala Asp
 85 90 95
 Asp Ser Glu Pro Thr Val Arg Ala Glu Leu Met Glu Gln Val Pro His
 100 105 110
 Ile Ala Leu Phe Cys Gln Glu Asn Arg Pro Ser Ile Pro Tyr Ala Phe
 115 120 125
 Ser Lys Tyr Leu Leu Pro Ile Val Val Arg Tyr Leu Ala Asp Gln Asn
 130 135 140
 Asn Gln Val Arg Lys Thr Ser Gln Ala Ala Leu Leu Ala Leu Leu Glu
 145 150 155 160
 Gln Glu Leu Ile Glu Arg Leu Asp Val Glu Thr Lys Val Cys Pro Val
 165 170 175
 Leu Ile Asp Leu Thr Ala Pro Asp Ser Asn Asp Asp Val Lys Thr Glu
 180 185 190

Ala	Val	Ala	Ile	Met	Cys	Lys	Met	Ala	Pro	Met	Val	Gly	Lys	Asp	Ile	195	200	205
Thr	Glu	Arg	Leu	Ile	Leu	Pro	Arg	Phe	Cys	Glu	Met	Cys	Cys	Asp	Cys	210	215	220
Arg	Met	Phe	His	Val	Arg	Lys	Val	Cys	Ala	Ala	Asn	Phe	Gly	Asp	Ile	225	230	235
Cys	Ser	Val	Val	Gly	Gln	Gln	Ala	Thr	Glu	Glu	Met	Leu	Leu	Pro	Arg	245	250	255
Phe	Phe	Gln	Leu	Cys	Ser	Asp	Asn	Val	Trp	Gly	Val	Arg	Lys	Ala	Cys	260	265	270
Ala	Glu	Cys	Phe	Met	Ala	Val	Ser	Cys	Ala	Thr	Cys	Gln	Glu	Ile	Arg	275	280	285
Arg	Thr	Lys	Leu	Ser	Ala	Leu	Phe	Ile	Asn	Leu	Ile	Ser	Asp	Pro	Ser	290	295	300
Arg	Trp	Val	Arg	Gln	Ala	Ala	Phe	Gln	Ser	Leu	Gly	Pro	Phe	Ile	Ser	305	310	315
Thr	Phe	Ala	Asn	Pro	Ser	Ser	Ser	Gly	Gln	Cys	Phe	Lys	Asp	Glu	Ser	325	330	335
Lys	Ser	Ser	Glu	Asp	Lys	Asp	Arg	Ile	Arg	Asp	Asp	Gly	Val	Val	Gln	340	345	350
Glu	Glu	Gln	Ser	Arg	Pro	Glu	Asp	Ala	Pro	Ser	Asp	Leu	Ser	Ala	Pro	355	360	365
His	Ser	Ser	Ala	Arg	Leu	Asp	Gly	Thr	Leu	Glu	Gly	Cys	Ala	Ala	Glu	370	375	380
Thr	Pro	Gly	Asp	Ser	Ala	Gly	Asp	Met	Arg	Val	Pro	Ala	Asp	Ser	Ser	385	390	395
Leu	Leu	Cys	Thr	Leu	Ser	Ser	Glu	Ser	Pro	Gln	Glu	Ala	Ala	Ser	Asp	405	410	415
Ala	Glu	Ser	Gly	Lys	Lys	His	Asp	Asn	Asn	Ser	Lys	Ser	Ala	Ser	Arg	420	425	430
Pro	Asp	Val	Gly	Thr	Ser	Ser	Pro	Glu	Pro	Thr	Pro	Leu	Asp	Gln	Glu	435	440	445
Met	Phe	Asn	Ser	Phe	His	Phe	Trp	Arg	Thr	Pro	Leu	Pro	Gln	Ile	Asp	450	455	460
Leu	Asp	Lys	Glu	Leu	Gln	Gln	Asp	Pro	Gly	Glu	Arg	Pro	Ser	Pro	Glu	465	470	475
Arg	Thr	Gly	Asp	Ala	Pro	Ala	Ala	Pro	Val	Pro	Gly	Ser	Pro	Ser	Ile	485	490	495

Thr	Met	Ala	Thr	Arg	Lys	Glu	Leu	Glu	Met	Ile	Glu	Asn	Leu	Glu	
			500					505				510			
Pro	His	Met	Asp	Asp	Pro	Asp	Val	Lys	Ala	Gln	Val	Glu	Val	Leu	Ser
		515					520					525			
Ala	Ala	Leu	Arg	Ala	Ser	Thr	Leu	Asp	Ala	His	Asp	Glu	Ala	Gly	Gly
		530				535					540				
Ala	Glu	Gln	Arg	Ser	Glu	Leu	Gln	Asp	Asp	Ala	Val	Gly	Ala	Gly	Gly
545				550					555						560
Glu	Leu	Pro	Asn	Cys	Ser	Ile	Ser	Glu	Asp	Thr	Ser	Glu	Pro	Leu	Val
			565						570					575	
Ile	Ala	Ala	Glu	Glu	Asn	Met	Glu	Ala	Thr	Pro	Asp	Tyr	Ile	His	Gly
			580					585					590		
Gly	Ala	Asp	Val	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Phe	Ser	Pro	Asp	Glu
		595					600					605			
Glu	Arg	Arg	Pro	Lys	Val	Gln	Asp	Val	Val	Pro	Gln	Ala	Leu	Leu	Asp
		610				615					620				
Gln	Tyr	Leu	Ser	Met	Thr	Asp	Pro	Ser	Arg	Ala	Gln	Thr	Val	Asp	Thr
625				630						635					640
Glu	Ile	Ala	Lys	His	Cys	Ala	Tyr	Ser	Leu	Pro	Gly	Val	Ala	Leu	Thr
				645					650					655	
Leu	Gly	Arg	Gln	Asn	Trp	His	Cys	Leu	Arg	Glu	Thr	Tyr	Glu	Thr	Leu
			660					665					670		
Ala	Ser	Asp	Met	Gln	Trp	Lys	Val	Arg	Arg	Thr	Leu	Ala	Phe	Ser	Ile
		675					680					685			
His	Glu	Leu	Ala	Val	Ile	Leu	Gly	Asp	Gln	Leu	Thr	Ala	Ala	Asp	Leu
		690				695					700				
Val	Pro	Ile	Phe	Asn	Gly	Phe	Leu	Lys	Asp	Leu	Asp	Glu	Val	Arg	Ile
705				710						715					720
Gly	Val	Leu	Lys	His	Leu	His	Asp	Phe	Leu	Lys	Leu	Leu	His	Ile	Asp
				725				730						735	
Lys	Arg	Arg	Glu	Tyr	Leu	Tyr	Gln	Leu	Gln	Glu	Phe	Leu	Val	Thr	Asp
			740					745					750		
Asn	Ser	Arg	Asn	Trp	Arg	Phe	Arg	Ala	Glu	Leu	Ala	Glu	Gln	Leu	Ile
		755					760					765			
Leu	Leu	Leu	Glu	Leu	Tyr	Ser	Pro	Arg	Asp	Val	Tyr	Asp	Tyr	Leu	Arg
		770				775					780				
Pro	Ile	Ala	Leu	Asn	Leu	Cys	Ala	Asp	Lys	Val	Ser	Ser	Val	Arg	Trp
785				790						795					800

Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys Leu His Met Ala
 805 810 815
 Thr Pro Pro Thr Phe Gly Val Glu Leu Ile Asn Glu Leu Val Glu Asn
 820 825 830
 Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala Phe Val Phe Val
 835 840 845
 Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met Asp Gln Phe Ala
 850 855 860
 Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn Asp Arg Val Pro
 865 870 875 880
 Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln Thr Leu Leu Glu
 885 890 895
 Lys Glu Tyr Phe Leu Ala Ser Ala Ser Cys His Gln Glu Ala Val Glu
 900 905 910
 Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser Asp Val Lys Tyr
 915 920 925
 Phe Ala Ser Ile His Pro Ser Ser Thr Lys Leu Ser Glu Asp Ala Met
 930 935 940
 Ser Thr Ala Ser Ser Thr Tyr
 945 950

<210> 13

<211> 1132

<212> DNA

<213> RATTUS NORVEGICUS

<400> 13

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atatccacat	ttgctaatec	atcaagctcg	ggccagtgtc	tcaaagatga	gagcaaaagc	180
tcagaagaca	aagacaggat	cagagacgat	ggtgtgtgtac	aagaagagca	gagcaggcca	240
gaggacgcac	cttcagacct	cagtgccect	cactccagtg	ccaggctgga	cggcacactt	300
gaaggetgtg	ctgccgagac	gcctggggac	tctgcaggtg	acatgcgtgt	tccagcggac	360
agctccttac	tctgtacttt	gtcctcagag	tctcctcagg	aagcagctag	tgacgctgag	420
agtggtaaaa	agcacgataa	caacagcaag	tctgcgtccc	ggccagacgt	tggcaccagc	480
tccccagagc	ccactccctt	agatcaggaa	atgttcaact	ccttccattt	ctggaggact	540
cctctacccc	agatagatct	tgataaagag	ctccaacagg	accctgggga	gaggcccagc	600
ccagagagaa	caggagatgc	acctgcagcc	cctgtaccag	gttctcccag	tatcaccatg	660
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cacgacgagg	ctggcgggtgc	agagcagcgg	agtgaactgc	aggacgacgc	agtggtgtcc	840
ggcggcgagc	ttccaaactg	tagcatcagc	gaagacactt	ctgagcctct	ggtcacgcct	900
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gacaccgaga	tcgctaagca	ctgtgcatac	agtctgcgcg	gtgtggctct	ga	1132